IN THE CLAIMS:

1. (currently amended) A method for determining lymphocyte diversity in a subject, said method comprising

a) providing:

i) labeled nucleic acid molecules from a population of said subject's lymphocytes, wherein said population of said subject's lymphocytes are from said subject after a bone marrow transplantation, wherein each of said labeled nucleic acid molecule encodes a lymphocyte receptor or a portion thereof,

ii) a population of nucleic acid molecules, wherein said population of nucleic acid molecules comprises random nucleic acid molecules or unselected express sequence tags, wherein said nucleic acid molecules within said population are attached to a solid substrate, ~~and wherein said solid substrate comprises a plurality of discrete regions, wherein each of said discrete regions comprises a different random nucleic acid molecule or an unselected express sequence tag,~~ and

iii) a standard curve generated by hybridizing said population of nucleic acid molecules with two or more different samples each containing a known number of variant nucleic acid molecules, wherein said standard curve provides the frequency of hybridization versus the number of variants present;

b) hybridizing said labeled nucleic acid molecules or fragments of said labeled nucleic acid molecules with said population of nucleic acid molecules;

c) assessing hybridization of said labeled nucleic acid molecules with said population of nucleic acid molecules to determine the frequency of hybridization ~~in each of said discrete regions~~, ~~and~~

d) comparing said frequency of hybridization to said standard curve in order to quantify the amount lymphocyte diversity in said subject, and

e) comparing said amount of lymphocyte diversity to said subject's baseline lymphocyte diversity before said bone marrow transplantation.

2. (cancelled)

3. (previously presented) The method of claim 1, wherein said solid substrate is a multiwell plate or membrane, a glass slide, a chip, or a bead.

4. (previously presented) The method of claim 1, wherein said solid substrate is a bead.

5. (original) The method of claim 4, wherein hybridization is assessed by flow cytometry.

6. (cancelled)

7. (previously presented) The method of claim 1, wherein said labeled nucleic acid molecules are labeled with a fluorochrome.

8. (original) The method of claim 7, wherein said fluorochrome is fluorescein isothiocyanate (FITC), phycoerythrin (PE), allophycocyanin (APC), or peridinin chlorophyll protein (PerCP).

9. (withdrawn; previously presented) The method of claim 1, wherein said labeled nucleic acid molecules are labeled with biotin.

10. (withdrawn; previously presented) The method of claim 1, wherein said labeled nucleic acid molecules are labeled with an enzyme.

11-12. (cancelled)

13. (original) The method of claim 1, wherein said population of lymphocytes are T lymphocytes.

14. (previously presented) The method of claim 13, wherein said labeled nucleic acid molecules encode a variable region from a T cell receptor.

15. (previously presented) The method of claim 13, wherein said labeled nucleic acid molecules encode a complementarity determining region (CDR) 3 β chain polypeptide.

16. (withdrawn) The method of claim 1, wherein said population of lymphocytes are B 1ymphocytes.

17. (withdrawn; previously presented) The method of claim 16, wherein said labeled nucleic acid molecules encode a variable region from a heavy chain or a light chain.

18-50. (cancelled)

51. (previously presented) The method of Claim 1, wherein said labeled nucleic acid molecules comprise labeled RNA molecules.

52. (previously presented) The method of Claim 1, wherein said labeled nucleic acid molecules comprise labeled DNA molecules.